

SEQUENCE LISTING

<110> BAYER AG

<120> Use of VLCFAE for identifying herbicidally
active compounds

<130> Le A 34 730

<140>

<141>

<160> 2

<170> PatentIn Ver. 2.1

<210> 1

<211> 2782

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (176)..(583)

<220>

<221> CDS

<222> (1119)..(1745)

<220>

<221> CDS

<222> (1821)..(2438)

<400> 1

acattaacta cctctcacca accaccaaac ccaatcccca caatattacc attactctca 60

tataactaca catattcata ttacatttt ttgccaacac aactccttat aagatatata
120

cttcatcaac ctatagatct cactcacata atcaacctac aaaacaaaaa caaga atg
178

Met
1

ggt aga tcc aac gag caa gat ctg ctc tct acc gag atc gtt aat cgt
226

Gly Arg Ser Asn Glu Gln Asp Leu Leu Ser Thr Glu Ile Val Asn Arg
5 10 15

ggg atc gaa cca tcc ggt cct aac gcc ggc tca cca acg ttc tcg gtt
274

Gly Ile Glu Pro Ser Gly Pro Asn Ala Gly Ser Pro Thr Phe Ser Val
20 25 30

agg gtc agg aga cgt ttg cct gat ttt ctt cag tcg gtg aac ttg aag
322

Arg Val Arg Arg Arg Leu Pro Asp Phe Leu Gln Ser Val Asn Leu Lys
35 40 45

tac gtg aaa ctt ggt tac cac tac ctc ata aac cat gcg gtt tat ttg
370

Tyr Val Lys Leu Gly Tyr His Tyr Leu Ile Asn His Ala Val Tyr Leu
50 55 60 65

gcg acc ata ccg gtt ctt gtg ctg gtt ttt agt gct gag gtt ggg agt
418
Ala Thr Ile Pro Val Leu Val Leu Val Phe Ser Ala Glu Val Gly Ser
70 75 80

tta agc aga gaa gag att tgg aag aag ctt tgg gac tat gat ctt gca
466
Leu Ser Arg Glu Glu Ile Trp Lys Lys Leu Trp Asp Tyr Asp Leu Ala
85 90 95

act gtt atc gga ttc ttc ggt gtc ttt gtt tta acc gct tgt gtc tac
514
Thr Val Ile Gly Phe Phe Gly Val Phe Val Leu Thr Ala Cys Val Tyr
100 105 110

ttc atg tct cgt cct cgc tct gtt tat ctt att gat ttc gct tgt tac
562
Phe Met Ser Arg Pro Arg Ser Val Tyr Leu Ile Asp Phe Ala Cys Tyr
115 120 125

aag ccc tcc gat gaa cac aag gtacgtccca acttttccat agaggaaata
613
Lys Pro Ser Asp Glu His Lys
130 135

gtctaaatta cttttaccca aaaaaaaaaa aaaaaaaaaa atctaaatta agtatactta
673

agaaattata attagatttg tcaaaaaata ataattataa ttagatggat tagttgttta
733

tagggctgcc taaataaaat aaaattttgc ctttgcattg gttacgttag taattatttt
793

tcaggtatat ataaaaagta attattttgc aaaaccttta gatattgggtt acgtttgatt
853

taaaaccgaa tggtttcgta gaaatttgag aaagtagata acctaaaaac tccgattaaa
913

gaaaccgggtt tgacttatat aattttaact ggtttctggtt ttcattttat tttataaaaa
973

aaacaatcca aatttacgac ctataatcaa aggagattga taggaaccgg actgataatt
1033

aatgaagct gaatcaaacc aaacaaaagt tcattttaatt ccggttctct cgggtttaat
1093

ctctttttgc attggattgg ttttag gtg aca aaa gaa gag ttc ata gaa cta
1145
Val Thr Lys Glu Glu Phe Ile Glu Leu
140 145

gcg aga aaa tca ggg aag ttc gac gaa gag aca ctc ggt ttc aag aag
1193
Ala Arg Lys Ser Gly Lys Phe Asp Glu Glu Thr Leu Gly Phe Lys Lys
150 155 160

agg atc tta caa gcc tca ggc ata ggc gac gag aca tac gtc cca aga
1241
Arg Ile Leu Gln Ala Ser Gly Ile Gly Asp Glu Thr Tyr Val Pro Arg

165	170	175
tcc atc tct tca tca gaa aac ata	aca acg atg aaa gaa ggt cgt gaa	
1289		
Ser Ile Ser Ser Ser Glu Asn Ile	Thr Thr Met Lys Glu Gly Arg Glu	
180	185	190
gaa gcc tct aca gtg atc ttt gga gca cta gac	gaa ctc ttc gag aag	
1337		
Glu Ala Ser Thr Val Ile Phe Gly Ala Leu Asp	Glu Leu Phe Glu Lys	
195	200	205
aca cgt gta aaa cct aaa gac gtt ggt gtc ctt	gtg gtt aac tgt agc	
1385		
Thr Arg Val Lys Pro Lys Asp Val Gly Val Leu Val Val	Asn Cys Ser	
210	215	220
att ttc aac ccg aca ccg tcg ttg tcc gca atg	gtg ata aac cat tac	
1433		
Ile Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Ile	Asn His Tyr	
230	235	240
aag atg aga ggg aac ata ctt agt tac aac ctt	gga ggg atg gga tgt	
1481		
Lys Met Arg Gly Asn Ile Leu Ser Tyr Asn Leu Gly Gly	Met Gly Cys	
245	250	255
tcg gct gga atc ata gct att gat ctt gct cgt	gac atg ctt cag tct	
1529		
Ser Ala Gly Ile Ile Ala Ile Asp Leu Ala Arg Asp	Met Leu Gln Ser	
260	265	270
aac cct aat agt tat gct gtt gtt gtg agt act	gag atg gtt ggg tat	
1577		
Asn Pro Asn Ser Tyr Ala Val Val Val Ser Thr Glu Met Val Gly Tyr		
275	280	285
aat tgg tac gtg gga agt gac aag tca atg gtt	ata cct aat tgt ttc	
1625		
Asn Trp Tyr Val Gly Ser Asp Lys Ser Met Val Ile Pro Asn Cys Phe		
290	295	300
ttt agg atg ggt tgt tct gcc gtt atg ctc tct	aac cgt cgt cgt gac	
1673		
Phe Arg Met Gly Cys Ser Ala Val Met Leu Ser Asn Arg Arg Arg Asp		
310	315	320
ttt cgc cat gct aag tac cgt ctc gag cac att	gtc cga act cat aag	
1721		
Phe Arg His Ala Lys Tyr Arg Leu Glu His Ile Val Arg Thr His Lys		
325	330	335
gct gct gac gac cgt agc ttc agg tttcattcat	tttggtatta attcggttta	
1775		
Ala Ala Asp Asp Arg Ser Phe Arg		
340	345	
caatctcttg accgacctag taactaattt tgtgtggttt	ttagg agt gtg tac cag	
1832		
	Ser Val Tyr Gln	
gaa gaa gat gaa caa gga ttc aag ggg ttg aag	ata agt aga gac tta	
1880		

Model	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Model	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

aatcaagtaa gatctctaatt tactccaacc aaaagataca gtttggttgg atgataggag
2518

ttatttactg atcattogta tctaagtctg ttataagaat ggatgtggct agagtcctgt
2578

ttagcttcaa cttgttttat tttttgtttg ttctctattg gatcttcata aactttgaga
2638

gattaaagaa aaaaactctt ctttagtttg atagaacaga tggtcattgt aatttcttta
2698

atatgtcaaa gtaaaacaat ttcttttttaa ggcaatctat attcagatac ataataaatt
2758

tagtttacgt gtataagaag atac
2782

 $\langle 210 \rangle$ 2

<211> 550

<212> PRT

<213> Arabidopsis thaliana

<400> 2

Met Gly Arg Ser Asn Glu Gln Asp Leu Leu Ser Thr Glu Ile Val Asn
1 5 10 15

Arg Gly Ile Glu Pro Ser Gly Pro Asn Ala Gly Ser Pro Thr Phe Ser
20 25 30

Val Arg Val Arg Arg Arg Leu Pro Asp Phe Leu Gln Ser Val Asn Leu
35 40 45

Lys Tyr Val Lys Leu Gly Tyr His Tyr Leu Ile Asn His Ala Val Tyr
50 55 60

Leu Ala Thr Ile Pro Val Leu Val Leu Val Phe Ser Ala Glu Val Gly
65 70 75 80

Ser Leu Ser Arg Glu Glu Ile Trp Lys Lys Leu Trp Asp Tyr Asp Leu
85 90 95 -

Ala Thr Val Ile Gly Phe Phe Gly Val Phe Val Leu Thr Ala Cys Val
100 105 110

Tyr Phe Met Ser Arg Pro Arg Ser Val Tyr Leu Ile Asp Phe Ala Cys
115 120 125

Tyr Lys Pro Ser Asp Glu His Lys Val Thr Lys Glu Glu Phe Ile Glu
130 135 140

Leu Ala Arg Lys Ser Gly Lys Phe Asp Glu Glu Thr Leu Gly Phe Lys
145 150 155 160

Lys Arg Ile Leu Gln Ala Ser Gly Ile Gly Asp Glu Thr Tyr Val Pro
165 170 175

Arg Ser Ile Ser Ser Ser Glu Asn Ile Thr Thr Met Lys Glu Gly Arg
180 185 190

Glu Glu Ala Ser Thr Val Ile Phe Gly Ala Leu Asp Glu Leu Phe Glu
195 200 205

Lys	Thr	Arg	Val	Lys	Pro	Lys	Asp	Val	Gly	Val	Leu	Val	Val	Asn	Cys	210	215	220
Ser	Ile	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Ile	Asn	His	225	230	235
Tyr	Lys	Met	Arg	Gly	Asn	Ile	Leu	Ser	Tyr	Asn	Leu	Gly	Gly	Met	Gly	245	250	255
Cys	Ser	Ala	Gly	Ile	Ile	Ala	Ile	Asp	Leu	Ala	Arg	Asp	Met	Leu	Gln	260	265	270
Ser	Asn	Pro	Asn	Ser	Tyr	Ala	Val	Val	Val	Ser	Thr	Glu	Met	Val	Gly	275	280	285
Tyr	Asn	Trp	Tyr	Val	Gly	Ser	Asp	Lys	Ser	Met	Val	Ile	Pro	Asn	Cys	290	295	300
Phe	Phe	Arg	Met	Gly	Cys	Ser	Ala	Val	Met	Leu	Ser	Asn	Arg	Arg	Arg	305	310	315
Asp	Phe	Arg	His	Ala	Lys	Tyr	Arg	Leu	Glu	His	Ile	Val	Arg	Thr	His	325	330	335
Lys	Ala	Ala	Asp	Asp	Arg	Ser	Phe	Arg	Ser	Val	Tyr	Gln	Glu	Glu	Asp	340	345	350
Glu	Gln	Gly	Phe	Lys	Gly	Leu	Lys	Ile	Ser	Arg	Asp	Leu	Met	Glu	Val	355	360	365
Gly	Gly	Glu	Ala	Leu	Lys	Thr	Asn	Ile	Thr	Thr	Leu	Gly	Pro	Leu	Val	370	375	380
Leu	Pro	Phe	Ser	Glu	Gln	Leu	Leu	Phe	Phe	Ala	Ala	Leu	Leu	Arg	Arg	385	390	395
Thr	Phe	Ser	Pro	Ala	Ala	Lys	Thr	Ser	Thr	Thr	Thr	Ser	Phe	Ser	Thr	405	410	415
Ser	Ala	Thr	Ala	Lys	Thr	Asn	Gly	Ile	Lys	Ser	Ser	Ser	Ser	Asp	Leu	420	425	430
Ser	Lys	Pro	Tyr	Ile	Pro	Asp	Tyr	Lys	Leu	Ala	Phe	Glu	His	Phe	Cys	435	440	445
Phe	His	Ala	Ala	Ser	Lys	Val	Val	Leu	Glu	Glu	Leu	Gln	Lys	Asn	Leu	450	455	460
Gly	Leu	Ser	Glu	Glu	Asn	Met	Glu	Ala	Ser	Arg	Met	Thr	Leu	His	Arg	465	470	475
Phe	Gly	Asn	Thr	Ser	Ser	Ser	Gly	Ile	Trp	Tyr	Glu	Leu	Ala	Tyr	Met	485	490	495
Glu	Ala	Lys	Glu	Ser	Val	Arg	Arg	Gly	Asp	Arg	Val	Trp	Gln	Ile	Ala	500	505	510
Phe	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Val	Val	Trp	Lys	Ala	Met	Arg	515	520	525
Lys	Val	Lys	Lys	Pro	Thr	Arg	Asn	Asn	Pro	Trp	Val	Asp	Cys	Ile	Asn	530	535	540

Arg Tyr Pro Val Pro Leu
545 550